

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 21:10:37 ; Search time 531.339 Seconds

(without alignments)
9201.802 Million cell updates/sec

Title: US-09-988-971-1_COPY_517_684

Perfect score: 168

Sequence: 1 gccacacgcgtgcccctg59.....gcccacgcgtgcccacgac 168

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
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16: em_fun: *
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36: em_hcg_mam: *
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39: em_higo_hum: *
40: em_higo_mus: *
41: em_higo_ther: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	100.0	737	9	AF290986 Homo sapi
2	168	100.0	786	9	AF290985 Homo sapi
3	168	100.0	786	9	AF326353 Homo sapi
4	168	100.0	2415	9	AK026545 Homo sapi
5	168	100.0	2567	6	AX452880 Sequence
6	166.4	99.0	1183	6	AX443133 Sequence
7	166.4	99.0	1183	6	AX443135 Sequence
8	124.8	74.3	1221	10	AF434990 Mus muscu
9	124.8	74.3	1348	10	AF287467 Mus muscu
10	90.8	54.0	66741	9	HS460J8
11	90.8	54.0	145833	2	AC026539 Homo sapi
12	83.8	49.9	145068	9	HS0397781
13	64.8	38.6	114096	2	AC123560 Homo sapi
14	64.8	38.6	168498	2	AC125701 Homo sapi
15	43.6	26.0	1518	9	HUMLYNXT
16	43.6	26.0	2298	9	HUMLYN
17	40	23.8	2044	10	MUSLYN
18	40	23.8	2703	10	MUSLYNB
19	40	23.8	2766	10	MUSLYNA
20	40	23.8	2938	10	BC031547 Mus muscu
21	39	23.2	1076	9	HS030473 Homo sapi
22	39	23.2	1870	9	BC007042 Homo sapi
23	39	23.2	2021	9	HS044403 Homo sapi
24	39	23.2	2109	6	AX428893 Sequence
25	39	23.2	2665	6	AX333017 Sequence
26	39	23.2	2665	6	DB9077
27	38.8	23.1	1538	10	RATLYNMYR
28	38.8	23.1	1601	10	RATLYNMYR
29	38.8	23.1	2041	10	RNAF000300
30	38.8	23.1	2032	10	RNAF000301
31	38.8	23.1	2824	10	RNAF000302
32	38.8	23.1	3458	10	RATLYNMYR
33	38	22.6	3701	5	CHRTCKL
34	38	22.6	4073	5	GGTKL
35	35.6	21.2	3921	5	XHCYES
36	35.2	21.0	38681	1	SC8D9
37	34.4	20.5	1527	9	SSC277921
38	34.4	20.5	2032	9	HS1CKB
39	34.4	20.5	2032	9	HUM1CKRA
40	34.4	20.5	139703	2	AC111951
41	34.4	20.5	173249	2	AC123468
42	34.4	20.5	180424	2	AC090496 Mus muscu
43	34.2	20.4	1619	9	AB049594 Ephydaria
44	34	20.2	2210	9	BC007371 Homo sapi
45	34	20.2	2235	9	HSBIRPTK

ALIGNMENTS

RESULT 1
AF290986 737 bp mRNA linear PRI 22-APR-2002
LOCUS AF290986
DEFINITION Homo sapiens Src-like adaptor protein-2 splice isoform mRNA.
ACCESSION AF290986
VERSION AF290986.1 GI:17351922
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 737)
Loreto M.P. and McGlade, C.J.
Direct Submission

JOURNAL Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

FEATURES

source

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/db_xref="taxon:9606"
/chromosome="20"
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1..737

CDS

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BASE COUNT 152 a 219 c 218 g 148 t

ORIGIN

Query Match 100.0%; Score 168; DB 9; Length 737;
Best Local Similarity 100.0%; Pred. No. 5.7e-33;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTGGCCCTGGGCGAGTTTCCCGGAGTGGCCGCGGAGCTGTGCTGAGA 60

Db 103 GCCACAGCCGTGGCCCTGGGCGAGTTTCCCGGAGTGGCCGCGGAGCTGTGCTGAGA 162

QY 61 CTGGGGAGCCATTGACATCGTCTGAGAGATGAGACTGATGAGCGTGTCTGAA 120

Db 163 CTGGGGAGCCATTGACATCGTCTGAGAGATGAGACTGATGAGCGTGTCTGAA 222

QY 121 GTCTCAGGCGAGAGTATTAACATCCCAAGCGTCCAGCTGGCCAAAGTC 168

Db 223 GTCTCAGGCGAGAGTATTAACATCCCAAGCGTCCAGCTGGCCAAAGTC 270

RESULT 2

AF290985

LOCUS AF290985 786 bp mRNA linear PRI 22-APR-2002

DEFINITION Homo sapiens Src-like adaptor protein-2 mRNA, complete cds.

ACCESSION AF290985.1 GI:17351920

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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CDS

BASE COUNT

162 a

234 c

231 g

159 t

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Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTGGCCCTGGGCGAGTTTCCCGGAGTGGCCGCGGAGCTGTGCTGAGA 60

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QY 61 CTGGGGAGCCATTGACATCGTCTGAGAGATGAGACTGATGAGCGTGTCTGAA 120

Db 163 CTGGGGAGCCATTGACATCGTCTGAGAGATGAGACTGATGAGCGTGTCTGAA 222

QY 121 GTCTCAGGCGAGAGTATTAACATCCCAAGCGTCCAGCTGGCCAAAGTC 168

Db 223 GTCTCAGGCGAGAGTATTAACATCCCAAGCGTCCAGCTGGCCAAAGTC 270

RESULT 3

AF26353

LOCUS AF26353 786 bp mRNA linear PRI 08-NOV-2001

DEFINITION Homo sapiens Src-like adaptor protein-2 mRNA, complete cds.

ACCESSION AF26353.1 GI:16797891

KEYWORDS

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/db_xref="taxon:9606"
/chromosome="20"
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/note="SLAP2; SH2 and SH3 domain-containing adaptor"
/codon_start=1
/product="Src-like adaptor protein-2"
/protein_id="AA129204.1"
/db_xref="GI:16797892"
/translation="WGSLSRRKSLPSPSSSSVGGQGVPTMEARSKATAVALGSP
AGGPAELSLRGEPLTIVSDGDMWTIVSEVSGEYNTSVHVAHSHGLVEGLSRE
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SPRLTFLQALVDHYSLADICCLKEPCVQAGAPLPGKDIPLVTVQRTPLNMK
ELDSILFSEAAVGESELSSEGLAESISFYSLINDEAVSLDA"

CDS

BASE COUNT

162 a

234 c

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159 t

ORIGIN

Query Match 100.0%; Score 168; DB 9; Length 786;
Best Local Similarity 100.0%; Pred. No. 5.7e-33;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTGGCCCTGGGCGAGTTTCCCGGAGTGGCCGCGGAGCTGTGCTGAGA 60

Db 103 GCCACAGCCGTGGCCCTGGGCGAGTTTCCCGGAGTGGCCGCGGAGCTGTGCTGAGA 162

QY 61 CTCGGGAGCCATTGACATCGTCTCTGAGATGAGACCTGTCGTCGTCTGAA 120
DB 163 CTCGGGAGCCATTGACATCGTCTCTGAGATGAGACCTGTCGTCGTCTGAA 222

QY 121 GTCCTAGGAGAGATTAACATCCCGAGCTGACGTCGCCAAAGTC 168
DB 223 GTCCTAGGAGAGATTAACATCCCGAGCTGACGTCGCCAAAGTC 270

RESULT 4
AK025645 2415 bp mRNA linear PRI 29-SEP-2000
LOCUS AK025645
DEFINITION Homo sapiens cDNA: FLJ21992, f18, clone HEP06554.
ACCESSION AK025645
VERSION AK025645.1 GI:10438227
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens hepatoma cell_line:Hepg2 cDNA to mRNA, clone_11b:HEP clone:HEP06554.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
TITLE NED0 human cDNA sequencing project
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2415)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

COMMENT NED0 human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5' - & 3' - end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES
source Location/Qualifiers
1. 2415
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/clone="HEP06554"
/cell_line="HepG2"
/cell_type="hepatoma"
/clone_11b="HEP"
/note="cloning vector pME18SFL3"
61..846
/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:10438228"

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SPRLTPSLQALVDHYSELADICLKEPCVLRAGPLGKXIDPLPTVQRTPLNMK
ELDSILFSEATCESILSEGLREISLFSYISLNDVAVSLDDA"

BASE COUNT 599 a 662 c 618 g 536 t

ORIGIN
Query Match 100.0%; Score 168; DB 9; Length 2415;
Best Local Similarity 100.0%; Pred. No. 5.2e-33;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTCGCTGGCAGATTCCCGCAGAGTGCCTGCTGCTGAGA 60
DB 163 GCCACAGCCGTCGCTGGCAGATTCCCGCAGAGTGCCTGCTGAGA 222

QY 61 CTCGGGAGCCATTGACATCGTCTCTGAGATGAGACCTGTCGTCGTCTGAA 120
DB 223 CTCGGGAGCCATTGACATCGTCTCTGAGATGAGACCTGTCGTCGTCTGAA 282

QY 121 GTCCTAGGAGAGATTAACATCCCGAGCTGACGTCGCCAAAGTC 168
DB 283 GTCCTAGGAGAGATTAACATCCCGAGCTGACGTCGCCAAAGTC 330

RESULT 5
AX452880 2567 bp DNA linear PAT 06-JUL-2002
LOCUS AX452880
DEFINITION Sequence 1 from Patent WO0242457.
ACCESSION AX452880
VERSION AX452880.1 GI:21712520
KEYWORDS
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Chang, H., Yang, W.-P., Wu, Y., Whitney, G.S., Perez-Villar, J. J. and Kanter, S. B.
TITLE Cloning and expression of human slap-2: a novel sh2/sh3 domain-containing human slap homologue having immune cell-specific expression
JOURNAL Patent: WO 0242457-A 1 30-MAY-2002;
Bristol-Myers Squibb Co. (US)
LOCATION/Qualifiers
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BASE COUNT 611 a 741 c 666 g 549 t

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.2e-33;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCACAGCCGTCGCTGGCAGATTCCCGCAGAGTGCCTGCTGCTGAGA 60
DB 517 GCCACAGCCGTCGCTGGCAGATTCCCGCAGAGTGCCTGCTGCTGAGA 576

QY 61 CTCGGGAGCCATTGACATCGTCTCTGAGATGAGACCTGTCGTCGTCTGAA 120
DB 577 CTCGGGAGCCATTGACATCGTCTCTGAGATGAGACCTGTCGTCGTCTGAA 636

QY 121 GTCCTAGGAGAGATTAACATCCCGAGCTGACGTCGCCAAAGTC 168
DB 637 GTCCTAGGAGAGATTAACATCCCGAGCTGACGTCGCCAAAGTC 684

RESULT 6
AX443133 1183 bp DNA linear PAT 02-JUL-2002
LOCUS AX443133
DEFINITION Sequence 74 from Patent WO0216599.
ACCESSION AX443133
VERSION AX443133.1 GI:21690555
KEYWORDS
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Burgess, C.E., Conley, P.B., Grose, W.M., Hart, M., Kekuda, R., Shumaker, R.A., Spytek, K.A., Szekeres, E.S., Tomlinson, J.E., Topper, J.N. and Yang, R.B.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0216599-A 74 28-FEB-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
LOCATION/Qualifiers
1..1183

BASE COUNT 251 a 359 c 333 g 240 t
 ORIGIN

Query Match 99.0%; Score 166.4; DB 6; Length 1183;
 Best Local Similarity 99.4%; Pred. No. 1.4e-32;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCACAGCCCTGGCCCTGGGAGATTTCCTCCGACAGGTGGCCCGCCGACGTGTCTGAGA 60
 DB 500 GCCACAGCCCTGGCCCTGGGAGATTTCCTCCGACAGGTGGCCCGCCGACGTGTCTGAGA 559
 QY 61 CTCGGGAGCCATTGACATTCCTCTCTGAGAGATGAGACTGGTGGCTGTCTGAA 120
 DB 560 CTCGGGAGCCATTGACATTCCTCTCTGAGAGATGAGACTGGTGGCTGTCTGAA 619
 QY 121 GTCTCAGGACAGAGATTAACATCCCGAGGCTCCAGCTGGCCAAAGTC 168
 DB 620 GTCTCAGGACAGAGATTAACATCCCGAGGCTCCAGCTGGCCAAAGTC 667

RESULT 7
 AX443135/c 1183 bp DNA linear PAT 02-JUL-2002
 LOCUS Sequence 76 from Patent WO0216599.
 DEFINITION AX443135
 ACCESSION AX443135
 VERSION AX443135.1 GI:21690556
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Burgess, C.E., Conley, P.B., Grose, W.M., Hart, M., Kekuda, R.,
 Shimkete, R.A., Speitek, K.A., Szekeres, E.S., Tomlinson, J.E.,
 Topper, J.N. and Yang, R.B.
 TITLE Proteins and nucleic acids encoding same
 JOURNAL Patent: WO 0216599-A 76 28-FEB-2002;
 Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
 FEATURES
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 /db_xref="taxon:9606"

BASE COUNT 240 a 333 c 359 g 251 t
 ORIGIN

Query Match 99.0%; Score 166.4; DB 6; Length 1183;
 Best Local Similarity 99.4%; Pred. No. 1.4e-32;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCACAGCCCTGGCCCTGGGAGATTTCCTCCGACAGGTGGCCCGCCGACGTGTCTGAGA 60
 DB 684 GCCACAGCCCTGGCCCTGGGAGATTTCCTCCGACAGGTGGCCCGCCGACGTGTCTGAGA 625
 QY 61 CTCGGGAGCCATTGACATTCCTCTCTGAGAGATGAGACTGGTGGCTGTCTGAA 120
 DB 624 CTCGGGAGCCATTGACATTCCTCTCTGAGAGATGAGACTGGTGGCTGTCTGAA 565
 QY 121 GTCTCAGGACAGAGATTAACATCCCGAGGCTCCAGCTGGCCAAAGTC 168
 DB 564 GTCTCAGGACAGAGATTAACATCCCGAGGCTCCAGCTGGCCAAAGTC 517

RESULT 8
 AF434990 1321 bp mRNA linear ROD 20-MAY-2002
 LOCUS AF434990
 DEFINITION Mus musculus Src-like adaptor protein-2 mRNA, complete cds.
 ACCESSION AF434990
 VERSION AF434990.1 GI:19242130
 KEYWORDS
 SOURCE Mus musculus.
 ORGANISM Mus musculus.

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1321)
 Pandey, A., Ibarrola, N., Kratchmarova, I., Fernandez, M.M.,
 Constantinescu, S.N., Ohara, O., Sawasdi, S., Lodish, H.F. and
 Mann, M.

TITLE A novel Src homology 2 domain-containing molecule, Src-like adaptor
 protein-2 (SLAP-2), which negatively regulates T cell receptor
 signaling
 JOURNAL U. Biol. Chem. 277 (21), 19131-19138 (2002)
 MEDLINE 22013997
 PUBMED 11891219

REFERENCE 2 (bases 1 to 1321)
 Ibarrola, N., Mann, M. and Pandey, A.
 TITLE Direct Submission
 JOURNAL Submitted (16-OCT-2001) Whitehead Institute for Biomedical
 Research, Nine Cambridge Center, Cambridge, MA 02142, USA
 FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:10090"
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BASE COUNT 298 a 381 c 363 g 279 t
 ORIGIN

Query Match 74.3%; Score 124.8; DB 10; Length 1321;
 Best Local Similarity 83.9%; Pred. No. 6.3e-22;
 Matches 141; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GCCACAGCCCTGGCCCTGGGAGATTTCCTCCGACAGGTGGCCCGCCGACGTGTCTGAGA 60
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 DB 433 CTCGGGAGCCATTGACATTCCTCTCTGAGAGATGAGACTGGTGGCTGTCTGAA 492
 QY 121 GTCTCAGGACAGAGATTAACATCCCGAGGCTCCAGCTGGCCAAAGTC 168
 DB 493 GTCTCAGGACAGAGATTAACATCCCGAGGCTCCAGCTGGCCAAAGTC 540

RESULT 9
 AF287467 1348 bp mRNA linear ROD 03-JUN-2002
 LOCUS AF287467
 DEFINITION Mus musculus Src-like adaptor protein-2 mRNA, complete cds.
 ACCESSION AF287467
 VERSION AF287467.1 GI:17351918
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1348)
 Loreto, M.P., Berry, D.M. and McGlade, C.J.
 TITLE Functional cooperation between c-Cbl and Src-like adaptor protein 2
 in the negative regulation of T-cell receptor signaling
 JOURNAL Mol. Cell. Biol. 22 (12), 4241-4255 (2002)
 MEDLINE 12024036
 PUBMED 12024036
 REFERENCE 2 (bases 1 to 1348)
 Loreto, M.P. and McGlade, C.J.
 TITLE Direct Submission

JOURNAL Submitted (14-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada

FEATURES

source Location/Qualifiers

1..1348
/organism="Mus musculus"
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/dev_stage="day 15 embryo"
282..1061
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/protein_id="AA138196.1"
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/note="Region: SH3 domain"

misc_feature

/note="Region: SH2 domain"

polysignal 1301..1306
BASE COUNT 324 a 385 c 362 g 277 t
ORIGIN

Query Match

Best Local Similarity 83.3%; Score 124.8; DB 10; Length 1348;

Matches 141; Conservative 0; Mismatch 27; Indels 0; Gaps 0;

Qy 1 GCCACAGCCGTGGCCCTGGCAGTTTCCCGCAGAGTGGCCGCCGAGCTGCTGAGA 60

Db 381 GTCACAGCTGTGGCCCTGGCAGTTTCCCGCAGAGTGGACAGCCGACATCTCTAGA 440

Qy 61 CTGGGGAGGACATTTGACCATCTGCTGAGATGAGACATGTCGTGTCTGAA 120

Db 441 CTGGGGAGGACCTGACATCTCTGAGATGAGATGTCGTGTGACATCCAGTCGGA 500

Qy 121 GTCTCAGGAGAGATTAACATCCCGCAGCTGCCAGTGGCCAAATGC 168

Db 501 GTCTCAGGAGAGATTAACATCCCGCAGCTGGTGTGTGCTAAATGC 548

RESULT 10

HS46038/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human DNA sequence from clone Rp3-46038 on chromosome 20q11.21-11.23 contains the 3' end of the gene for a novel protein similar to N-myc downstream regulated (NDRG1) the 5' end of a gene encoding a novel protein tyrosine kinase, ESTs, STS and GSSs, complete sequence.

AL031662
AL031662.26 GI:9716901
HTG; NDRG1; SH2 domain.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 66741)
Direct Submission
Submitted (23-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Aug 7, 2000 this sequence version replaced gi:6425549.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

FEATURES

source

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>
IMPORTANT: This sequence is not the entire insert of clone RP3-46038 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP3-46038 is at 66741 in this sequence. The true left end of clone RP3-46038 is at 41767 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP3-46038 is from the library RPI-3 constructed by the group of Pletier de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pCYPAC3.

Location/Qualifiers

1..66741
/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="20"

/map="q11.21-11.23"

/clone="RP3-46038"

/clone_1ib="RPI-3"

complement(50..544)

/note="match: GSS: Em:B45150"

complement(240..7128)

/gene="d0977B1.1"

complement(join(<240..339,6995..7128))

/gene="d0977B1.1"

/product="d046038.2 (novel protein tyrosine kinase with Src homology 2 (SH2) domain)"

/note="match: CDRAS: Em:AK025645

/evidence="not_experimental"

complement(join(<240..339,6995..7085))

/gene="d0977B1.1"

/note="Continues in Em:AL050318 as d0977B1.2"

/codon_start=1

/evidence="not_experimental"

/product="d046038.2 (novel protein tyrosine kinase with Src homology 2 (SH2) domain)"

/protein_id="CAC44645.1"

/db_xref="GI:15020830"

/translation="MGSLSRSKTSFSPSSSGPDQEPVSMOERHKTAVAGSFPAGEARLSLRGELTITISDDMMVTQSEVSEYHMPMSYVAKHGLYGLSREKAEELILPGNPGAFILRESQTRGCSYSLRSRPMWDRIHYH10RLDNGMLYISPLTFPPLHALVEHYSELADGICCPLEPCVLOKXGPIPGKDDPPVPTVPSLAWKKLDRSLPLEAPASGEASLSLSGASLSISLADPLDDA"

536..565

/note="15 copies 2 mer ag 93% conserved"

2375..2402

/note="14 copies 2 mer ta 100% conserved"

2783..3155

/note="match: GSS: Em:AQ807191"

complement(6983..7482)

/note="match: GSS: Em:AQ556467"

complement(6985..7492)

/note="match: GSS: Em:AQ556478"

7486..7925

/note="match: STS: Em:HS427015"

10615..10640

/note="13 copies 2 mer tt 92% conserved"

13593..13961

/note="MER21B repeat: matches 422..785 of consensus"

14248..14297

/note="MER21B repeat: matches 374..422 of consensus"

14594..14614

repeat_region

repeat_region /note="MER2B repeat: matches 355..374 of consensus"
14746..15078
/note="MER2B repeat: matches 1..355 of consensus"
polyA_site
complement(17516)
17519..17666
misc_feature
/note="match: GSS: Em:A2067993"
complement(17521)
complement(17522)
complement(17523)
complement(17533)
/gene="cd469A13.3"
/product="cd469A13.3" (continued from cd469A13.3 in
Em:AL132768")
/note="match: CDNA8: Em:AB033922 Em:U52073 Em:DB07953
Em:J92845 Em:AF004162 Em:U60593 Em:AF045664 Em:AB033921
Em:AF159092 Em:AF147402 Em:M58914
match: EST8: Em:AA718726 Em:AA023000 Em:AM003952 Em:W09263
Em:AA325826 Em:A1230962 Em:AA162360 Em:AA455016
Em:AV002395 Em:T85147 Em:A1786673 Em:AA113437 Em:A1004026
Em:H88707 Em:A1786673 Em:A1181197 Em:AA764653 Em:AA316771
Em:AU035165 Em:AV0023368"
/evidence=not experimental
complement(17542..17547)
/gene="cd469A13.3"
17555..17811
polyA_signal
/note="match: STS: Em:G139454"
join(13202..19451,22110..22282,26087..26127,30796..30847
/note="match: STS: Em:Q23762"
complement(join(19270..19451,20551..20589,22110..22161,
22247..22282,26087..26134,30796..30847,30966..31051,
32039..32142,37091..37147,46566..46652,48268..48328,
50163..50225,52342..53362,54429..54534))
/gene="nd469A13.3"
/note="nucleotide protein (F1J13556) similar to N-myc
downstream regulated (NDRG1)
match: proteins: SW:Q62433 SW:Q92597 Tr:O922L9 Sw:F97862"
/codon_start=1
/evidence=not experimental
/product="cd469A13.1 (continued from cd469A13.3 in
Em:AL132768)"
/protein_id="CA865625.1"
db_xref="taxid:330960"
/db_xref="taxid:330960"
/db_xref="taxid:330960"
/translation="EMDLETHGVVHTITGLPKRNPVILITHDGIMHSCNAFF
NFEWDQIYOHFAVDAGQGGBSPFPNGQYPMDEMAEALPVPLVTLISKSLT
HGFGDAAYLTLSRALHPHELVEGLVLINDPCKAKMDMAELASGLATVVNDITLA
HHFGESTLIQNLDITQYRMHIDIODINODINFLNSGNDELTERIIGDKTFKS
KLTKSGELIADWDSPAEVAEVENSRNLPTNTLLIKACDCGGIPDVVPKRLTEFK
YLQGMGYLYVULSHLSTESVPSASMTRLARSTRHTSSSLGSGSPSPSVTSNOS
DGTQGESPDVLDLHMOMVSC"
complement(24246..24780)
/gene="nd469A13.3"
/note="match: GSS: Em:A0592789"
complement(27990..28556)
/gene="nd469A13.3"
/note="match: GSS: Em:A0308867"
34313..34420
/note="HYI repeat: matches 1..109 of consensus"
34505..34560
/note="28 copies 2 mer ta 76% conserved"
34564..34611
/note="24 copies 2 mer ta 79% conserved"
42553..43658
/note="MER52C repeat: matches 1..1278 of consensus"
47989..48470
/note="match: GSS: Em:A062417"
49391..49480
/note="45 copies 2 mer ta 76% conserved"
52922..53120

[illegible]

TITLE JOURNAL COMMENT

ROY, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Strange-Thomann, N., Stojanovic, N., Subramaniam, A., Talamas, J.,
 Testa, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Veli, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 27, 2000 this sequence version replaced gi:7283243.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

 Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu

 Project Information
 Center project name: L7113
 Center clone name: 712_N_14

 Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960711
 Consensus quality: 125577 bases at least Q40
 Consensus quality: 135703 bases at least Q30
 Consensus quality: 135933 bases at least Q20
 Insert size: 182000; agarose- λ
 Insert size: 142233; sum-of- λ
 Quality coverage: 2.6 in Q20 bases; agarose- λ
 Quality coverage: 3.3 in Q20 bases; sum-of- λ

 NOTE: This is a 'working draft' sequence. It currently
 * consists of 37 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1214:	contig of 1214 bp in length	37528	37627:	gap of 100 bp
1315	1314:	gap of 100 bp	37628	40146:	contig of 2519 bp in length
1315	2673:	contig of 1359 bp in length	40147	40246:	gap of 100 bp
2674	2773:	gap of 100 bp	40247	43743:	contig of 3497 bp in length
2774	4520:	contig of 1747 bp in length	43744	43843:	gap of 100 bp
4521	4620:	gap of 100 bp	43844	47133:	contig of 3290 bp in length
4621	5961:	contig of 1341 bp in length	47134	47233:	gap of 100 bp
5962	6061:	gap of 100 bp	47234	51023:	contig of 3790 bp in length
6062	7719:	contig of 1658 bp in length	51024	51123:	gap of 100 bp
7720	7819:	gap of 100 bp	51124	54935:	contig of 3812 bp in length
7820	9789:	contig of 1980 bp in length	54936	55035:	gap of 100 bp
9800	9899:	gap of 100 bp	55036	59553:	contig of 4518 bp in length
9900	11434:	contig of 1535 bp in length	59554	59653:	gap of 100 bp
11435	11534:	gap of 100 bp	59654	64428:	contig of 4775 bp in length
11535	14382:	contig of 2848 bp in length	64429	64528:	gap of 100 bp
14383	14482:	gap of 100 bp	64529	69211:	contig of 4663 bp in length
14483	17148:	contig of 2666 bp in length	69212	69311:	gap of 100 bp
17149	17248:	gap of 100 bp	69312	72901:	contig of 3590 bp in length
17249	19239:	contig of 1991 bp in length	72902	73001:	gap of 100 bp
19240	19339:	gap of 100 bp	73002	76724:	contig of 3723 bp in length
19340	21102:	contig of 1763 bp in length	76725	76824:	gap of 100 bp
21103	21202:	gap of 100 bp	76825	81179:	contig of 4355 bp in length
21203	23371:	contig of 2169 bp in length	81180	81279:	gap of 100 bp
23372	23471:	gap of 100 bp	81280	87009:	contig of 5730 bp in length
23472	25782:	contig of 2311 bp in length	87010	87109:	gap of 100 bp
25783	25882:	gap of 100 bp	87110	90855:	contig of 3746 bp in length
25883	28824:	contig of 2942 bp in length	90856	90955:	gap of 100 bp
28825	28924:	gap of 100 bp	90956	96520:	contig of 5565 bp in length
28925	31619:	contig of 2695 bp in length	96521	96620:	gap of 100 bp
31620	31719:	gap of 100 bp	96621	102321:	contig of 5701 bp in length
31720	34679:	contig of 2960 bp in length	102322	102421:	gap of 100 bp
34680	34779:	gap of 100 bp	102422	108293:	contig of 5872 bp in length
34780	37527:	contig of 2748 bp in length	108294	108393:	gap of 100 bp

FEATURES

source	1. .145833
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="20"
	/map="20"
	/clone_id="RP11-712N14"
	/clone_lib="RPCT-11 Human Male BAC"
misc_feature	1. .1214
	/note="assembly_fragment"
misc_feature	1315. .2673
	/note="assembly_fragment"
misc_feature	2774. .4520
	/note="assembly_fragment"
misc_feature	4621. .5961
	/note="assembly_fragment"
misc_feature	6062. .7719
	/note="assembly_fragment"
misc_feature	7820. .9799
	/note="assembly_fragment"
misc_feature	9900. .11434
	/note="assembly_fragment"
misc_feature	11535. .14382
	/note="assembly_fragment"
misc_feature	14483. .17148
	/note="assembly_fragment"
misc_feature	17249. .19239
	/note="assembly_fragment"
misc_feature	19340. .21102
	/note="assembly_fragment"
misc_feature	21203. .23371
	/note="assembly_fragment"
misc_feature	23472. .25782
	/note="assembly_fragment"

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misc_feature /note="assembly_fragment"
25883..28824
/note="assembly_fragment"
28925..31619
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31720..34679
/note="assembly_fragment"
34780..37527
/note="assembly_fragment"
37628..40146
/note="assembly_fragment"
40247..43743
/note="assembly_fragment"
43844..47133
/note="assembly_fragment"
47234..51023
/note="assembly_fragment"
51124..54935
/note="assembly_fragment"
vector_side:right"
55036..59553
/note="assembly_fragment"

```

```

Query Match 54.0%; Score 90.8; DB 2; Length 145833;
Best Local Similarity 93.1%; Pred. No. 2,1e-13;
Matches 95; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 GCCACAGCCGTGGCCCTGGGAGGAGTTCCCGGAGTGCGCGGAGAGTGTGCTGAGA 60
DB 130655 GCCACAGCCGTGGCCCTGGGAGGAGTTCCCGGAGTGCGCGGAGAGTGTGCTGAGA 130714
QY 61 CTCGGGAGCCATTGACATCGTCTCTGAGAGTGAAGAGACTGG 102
DB 130715 CTCGGGAGCCATTGACATCGTCTCTGAGTGAAGAGACTGG 130756

```

```

RESULT 12
HSDJ977B1/c 145068 bp DNA linear PRI 20-JUL-2001
LOCUS HSDJ977B1
DEFINITION Human DNA sequence from clone RPS-977B1 on chromosome 20 contains
ESTs, STSs, GSSs and three putative Cpg islands. Contains the 3'
end of the gene for a novel protein tyrosine kinase, a
heterogeneous nuclear ribonucleoprotein A3 pseudogene, the gene for
three isoforms of a novel protein similar to putative
RAB5-interacting protein, the TGIF2 gene for TGF(beta)-induced
transcription factor 2 with two isoforms, the MYR12 gene for myosin
regulatory light chain 2 (smooth muscle isoform), the 3' end of the
gene KIAA0964 (ortholog of rat PSD-95/SAP90-associated protein 4)
with two isoforms and a novel gene, complete sequence.

```

```

ACCESSION AL050318.13 GI:5981785
VERSION HTG; Cpg island; heterogeneous ribonucleoprotein; KIAA0964; myosin
KEYWORDS regulatory light chain; MYR12; RAB5-interacting protein; SH2
domain; TGIF2; transcription factor; tyrosine kinase.

```

```

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 145068)
Lloyd, D.

```

```

REFERENCE Direct Submission
AUTHORS Submitted (19-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
TITLE CB10 15A, UK, E-mail enquiries: humgeny@anger.ac.uk; uk clone
JOURNAL requests: clonerequests@sanger.ac.uk

```

COMMENT

On Jul 28, 2000 this sequence version replaced gi:5924017. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession

FEATURES

source

numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
 from the WORMPEP database can be found at
<http://www.sanger.ac.uk/projects/C.elegans/wormpep> This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 20, constructed by the Sanger Centre Chromosome 20
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr20>
 This sequence is the entire insert of clone RPS-977B1. The true left
 end of clone RPS-46018 is at 63245 in this sequence. The true right
 end of clone CTD-218219 is at 62218 in this sequence. This sequence
 was finished as follows unless otherwise noted: all regions were
 either double-stranded or sequenced with an alternate chemistry or
 covered by high quality data (i.e., phred quality >= 30); an
 attempt was made to resolve all sequencing problems, such as
 compressions and repeats: all regions were covered by at least one
 plasmid subclone or more than one M13 subclone; and the assembly
 was confirmed by restriction digest. RPS-977B1 is from the library
 RPCI-5 constructed by the group of Pieter de Jong. For further
 details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pCYPAC2.

Location/Qualifiers

```

1..145068
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RPS-977B1"
/clone_1b="RPCI-5"
568..875
/note="AluX repeat: matches 1..311 of consensus"
1024..1580
/note="match: GSS: Em:A0620498"
1047..1629
/note="match: GSS: Em:A0779162"
1631..1923
/note="AluSg repeat: matches 1..294 of consensus"
2776..2842
/note="L2 repeat: matches 2357..2423 of consensus"
3891..3949
/note="MIR repeat: matches 34..90 of consensus"
4458..4611
/note="MIR repeat: matches 67..231 of consensus"
5133..5549
/note="L1MD2 repeat: matches 5924..6340 of consensus"
5550..5680
/note="FLAM_C repeat: matches 1..132 of consensus"
5703..5890
/note="AluSg repeat: matches 120..308 of consensus"
5923..6012
/note="AluX repeat: matches 5432..5528 of consensus"
6588..6889
/note="AluSg repeat: matches 1..303 of consensus"
join(7423..7784,9960..10039,10306..10394,10917..11329,
34968..35059,36569..36724,37531..39351)
/gene="KIAA0964"
join(67423..7784,9960..10039,10917..11329,34968..35059,
36569..36724,37531..39351)
/gene="KIAA0964"
/product="dJ977B1.6.2 (KIAA0964 (ortholog of rat
PSD-95/SAP90-associated protein 4))"
/feature="match: cDNAs: Em:U67140 Em:AB000277 Em:AB000276
Em:AB000275 Em:AB023181 Em:AF009204 Em:AB003594 Em:U67988
Em:U67137 Em:U67138 Em:U67987 Em:AF131778
match: ESTs: Em:AI81867 Em:AI620816 Em:AA496750
Em:AA647532 Em:AI747584 Em:AA931146 Em:AI887761"

```


[illegible]

	repeat_region	12084..12121	/note="l2 repeat: matches 2661..2692 of consensus"
	repeat_region	12631..12714	/note="HALI repeat: matches 1589..1665 of consensus"
	repeat_region	13077..13367	/note="Aluo repeat: matches 3..220 of consensus"
	repeat_region	13440..13742	/note="AlusX repeat: matches 1..304 of consensus"
	repeat_region	13932..14197	/note="L1MB7 repeat: matches 5915..6173 of consensus"
	repeat_region	14198..14512	/note="AluY repeat: matches 1..307 of consensus"
	repeat_region	14513..14756	/note="L1MB7 repeat: matches 5650..5915 of consensus"
	repeat_region	14789..15705	/note="L1MB4 repeat: matches 5162..6185 of consensus"
	repeat_region	15706..16004	/note="AlusG repeat: matches 1..298 of consensus"
	repeat_region	16005..16060	/note="L1MB4 repeat: matches 5111..5162 of consensus"
	Query Match	49.9%; Score 83.8; DB 9; Length 145068;	
	Best Local Similarity	76.3%; Pred. No. 1,3e-11; Indels 0; Gaps 0;	
	Matches 103; Conservative	0; Mismatches 32; Indels 0; Gaps 0;	
Qy	34	GATGGCCCCCGCAGACGTGCTGCCTGAAGACTCGGGAGACCATTGACCATGCTCTTGAGGAT	93
Db	144403	GTGTGTGGGGCCCTTGTGGCTCATCTGAAGAAGAGTCGCCCACTCTTTCTCTTCACGGGAT	144344
Qy	94	GGAACCTGCTGACGACGCGTCGTCTGAATCTCAGGAGAGATTAACATCCCAGCGTC	153
Db	144343	GGAACTGCGTGGACGGTGGCTGTGAAGTCTCAGGACGAGGTATAACATCCCAGCGTC	144284
Qy	154	CACGTGGCCCAAAGTC	168
Db	144283	CACGTGGCCCAAAGTC	144269
RESULT 13			
LOCUS	AC123560	114096 bp	DNA linear HTG 23-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-61G22, *** SEQUENCING IN PROGRESS		
ACCESSION	AC123560		
VERSION	AC123560.2	GI:21908372	
KEYWORDS	HTG; HTGS PHASE1.		
SOURCE	Rattus norvegicus.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 114096)		
AUTHORS	Murray,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alibrooks,S.L., Amaratunge,H.C., Aye,J.R., Ayel,M., Banks,T., Barbieri,J.J., Benton,J., Blinake,K., Blankenburg,K., Bonnin,D., Bouck,J., Bouché,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P., Bunney,C., Burne,P., Burkette,C., Butrell,K.L., Byrd,N.C., D. Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., DeJamey,K.R., Delgado,O., Denn,A.L., Ding,Y., Din,H.H., Donthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Fallis,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P., Gabriel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guvera,M., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huijx,S., Humey,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Joliver,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryah,J., Kovar,C., Kratovic,J., Kuresti,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,		

Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
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 Weinreb, G., and Gibbs, R.

Unpublished
 Direct Submission
 2 (bases 1 to 114096)
 Morley, K.C.

Submitted (31-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 114096)
 Morley, K.C.

Direct Submission
 Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 19, 2002 this sequence version replaced gi:21281284.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

Project Information
 Center project name: GXON
 Center clone name: CH230-61G22

Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 92427 bases at least Q40
 Consensus quality: 95724 bases at least Q30
 Consensus quality: 98040 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 33 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

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 5446 6562: contig of 1117 bp in length
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 7725 7825: gap of unknown length
 10040: contig of 2216 bp in length

10041 10140: gap of unknown length
 10141 11624: contig of 1486 bp in length
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 13317 13416: gap of unknown length
 13417 14590: contig of 1174 bp in length
 14591 14690: gap of unknown length
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 73288 81837: contig of 8450 bp in length
 81838 81837: gap of unknown length
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FEATURES
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 /db_xref="taxon:10116"
 /clone="CH230-61G22"

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 Best Local Similarity 78.0%; Pred. No. 9.9e-07;
 Matches 78; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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 DB 54903 GTCCGGAGACATGATCATGATCTGAGTGAAGTCTACT 54942

RESULT 14
AC125701
LOCUS
DEFINITION
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Rattus norvegicus clone CH230-12L23, *** SEQUENCING IN PROGRESS
***, 56 unordered pieces.
AC125701
AC125701.3 GI:22004133
HTG: HTGS PHASE1.
SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 168498)
Nuzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaralunge,H.C., Are,J.R., Ayelle,M., Banks,T.,
Barbata,J., Benton,J., Bimage,K., Blankenburg,K., Bonini,D.,
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Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
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Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dink,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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Wainstock,G. and Gibbs,R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
2 (bases 1 to 168498)
Unpublished
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168498)
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 30, 2002 this sequence version replaced gi:22002395.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center Project name: GDYR
Center Clone name: CH230-12L23
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 126947 bases at least Q40
Consensus quality: 134611 bases at least Q30
Consensus quality: 140704 bases at least Q20

NOTE: Batted insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 56 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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Query Match 38.6%; Score 64.8; DB 2; Length 168498;

Best Local Similarity 78.0%; Pred. No. 9.5e-07; Indels 0; Gaps 0;

Matches 78; Conservative 0; Mismatches 22;

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RESULT 15
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 LOCUS HUMLYNTK 1518 bp mRNA linear PRI 21-MAR-1997

DEFINITION Human Lyn B protein mRNA, complete cds.
 ACCESSION M79321
 VERSION M79321.1 GI:187270
 KEYWORDS lyn protein; tyrosine kinase.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1518)
 Rider, L.G., Raben, N., Miller, L. and Jalsensma, C.
 The cDNAs encoding two forms of the lyn protein tyrosine kinase are expressed in rat mast cells and human myeloid cells

JOURNAL MEDLINE 94171041
 PUBMED 8125304
 REFERENCE 2 (bases 1 to 1518)
 MILLER, L.R. and Jalsensma, C.L.
 Human promyeloid cells express two forms of the lyn protein tyrosine kinase

FEATURES
 source Unpublished
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Matches 76; Conservative 0; Mismatches 54;

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QY 159 GGCCCAAGTC 168
 Db 315 GGCCCAAGTC 324

Search completed: March 30, 2003, 06:25:59
 Job time : 618.589 secs